

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.6  
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OM proteoin - proteoin search, using sw model

Run on: October 24, 2005, 13:10:07 ; Search time 170 Seconds  
(without alignments)  
659,678 Million cell updates/sec

Title: US-10-733-288b-4

Perfect score: 1142  
Sequence: 1 IYGGRRARHAMPFWISLQ.....PDAPFAVQAQFVWKIDSIQR 219

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1142	100.0	267	1	ELNE_HUMAN
2	905	79.2	282	1	Q8MJD1
3	873.5	76.5	285	2	Q61515
4	686	60.1	258	2	Q9GME1
5	659	57.7	207	2	Q92284
6	657	57.5	145	2	Q6LDP5
7	648.5	56.8	254	2	Q8K597
8	647.5	56.7	256	1	PRN3_HUMAN
9	646.5	56.6	237	2	Q6LBR2
10	644.5	56.4	234	1	PRN3_MOUSE
11	584.5	51.2	245	2	Q6DF10
12	489	42.8	251	1	CAP7_HUMAN
13	437	38.3	219	1	CAP7_PIG
14	392	34.3	264	2	Q8QGF6
15	392	34.3	264	2	Q6GPF5
16	387	33.9	258	2	Q867B0
17	384	33.6	265	2	Q66KX6
18	381	33.4	283	2	Q6UWY2
19	379	33.2	265	2	Q7SYX8
20	379	33.2	266	1	EL1_PIG
21	370.5	32.4	268	1	Q9W702
22	370	32.4	268	2	Q61SW6
23	369	32.3	258	1	EL1_HUMAN
24	366	32.0	266	2	Q91X79
25	365	32.0	266	1	EL1_RAT
26	364	31.9	265	2	Q6GNC0
27	364	31.9	266	2	Q9D936
28	360.5	31.6	249	2	Q9W701
29	358	31.3	245	1	MCT1_SHEEP
30	358	31.3	266	2	O46644
31	357	31.3	266	1	EL1_BOVIN

32	355	31.1	226	2	Q86SR2	Q86SR2 homo sapien
33	355	31.1	251	2	Q6GJN2	Q6GJN2 bos taurus
34	354	31.0	278	2	Q6BFN6	Q6BFN6 brachydanio
35	353.5	31.0	261	1	CAT6_MOUSE	P28293 mus musculus
36	351.5	30.8	262	1	GRAA_HUMAN	P12544 homo sapien
37	351.5	30.8	266	2	Q6AZC0	Q6AZC0 brachydanio
38	350.5	30.7	267	2	Q6DGM4	Q6DGM4 brachydanio
39	349.5	30.6	226	1	DDN1_BOVIN	P80219 bos taurus
40	349	30.6	260	2	Q7SE23	Q7SE23 gallus gall
41	348.5	30.5	236	2	Q7S1G3	Q7S1G3 salmo salar
42	346.5	30.3	255	1	CAT6_HUMAN	P08311 homo sapien
43	342	29.9	269	2	Q6AZF9	Q6AZF9 xenopus lae
44	340.5	29.8	257	1	GRAM_HUMAN	P51124 homo sapien
45	339.5	29.7	260	1	GRAA_MOUSE	P11032 mus musculus

## ALIGNMENTS

RESULT 1	ELNE_HUMAN	STANDARD;	PRT;	267 AA.
AC	P08246; P09649;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Leukocyte elastase precursor (EC 3.4.21.37) (Neutrophil elastase) (PMN elastase) (Bone marrow serine protease) (Medullasin).			
GN	Name=ELA2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=89374820; PubMed=2775493;			
RA	Farley D., Travis J., Salvesen G.;			
RT	"the human neutrophil elastase gene. Analysis of the nucleotide sequence reveals three distinct classes of repetitive DNA.";			
RL	Biol. Chem. Hoppe-Seyler 370:737-744 (1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=88067782; PubMed=3479752;			
RA	Nakanura H., Okano K., Aoki Y., Shimizu H., Naruto M.;			
RT	"Nucleotide sequence of human bone marrow serine protease (medullasin) gene.";			
RL	Nucleic Acids Res. 15:9601-9601 (1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=89008342; PubMed=2902087;			
RA	Takahashi H., Nuklwa T., Yoshimura K., Quick C.D., States D.J.,			
RT	Holmes M.D., Whang-Peng J., Knutsen T., Crystal R.G.;			
RT	"Structure of the human neutrophil elastase gene.";			
RL	J. Biol. Chem. 263:14739-14747 (1988).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=90211319; PubMed=2322278;			
RA	Okano K., Aoki Y., Shimizu H., Naruto M.;			
RT	"Functional expression of human leukocyte elastase (HLE)/medullasin in eukaryotic cells.";			
RL	Biochem. Biophys. Res. Commun. 167:1326-1332 (1990).			
RN	[5]			
RP	SEQUENCE FROM N.A., AND VARIANTS ILE-219; LEU-257 AND LEU-262.			
RA	Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,			
RA	Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,			
RT	Sherwood J.K., Sherwood A.M., Leithausen B.J., Nickerson D.A.;			
RT	"NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://esp.gs.washington.edu).";			
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE OF 30-267 FROM N.A.			
RA	MEDLINE=88032918; PubMed=2822677;			
RA	Okano K., Aoki Y., Sakurai T., Kajitani M., Kanai S., Shimazu T.,			

RA Shimizu H., Naruto M.;  
 RT "Molecular cloning of complementary DNA for human medullasin: an  
 RT inflammatory serine protease in bone marrow cells."; *Proc. Natl. Acad. Sci. U.S.A.* 102:13-16(1987).  
 RN [17]  
 RN SEQUENCE OF 75-267 FROM N.A.  
 RA MEDLINE=88115408; PubMed=3422232;  
 RA Takahashi H., Nukitwa T., Baasat P.;  
 RT "Myelomonocytic cell lineage expression of the neutrophil elastase  
 RT gene."; *Biol. Chem.* 263:2543-2547(1988).  
 RN [18]  
 RN SEQUENCE OF 30-247.  
 RA MEDLINE=87175647; PubMed=3550808;  
 RA Sinha S., Matorek W., Kerr S., Giles J., Bode W., Travis J.;  
 RT "Primary structure of human neutrophil elastase."; *Proc. Natl. Acad. Sci. U.S.A.* 84:2228-2232(1987).  
 RN [19]  
 RN SEQUENCE OF 262-267.  
 RA MEDLINE=91315473; PubMed=1859409;  
 RA Aoki Y., Hase T.;  
 RT "The primary structure and elastolytic activity of medullasin (a  
 RT serine protease of bone marrow)."; *Biochem. Biophys. Res. Commun.* 178:501-506(1991).  
 RN [110]  
 RN PRELIMINARY SEQUENCE OF 30-103.  
 RA Travis J., Giles P.J., Porcelli L., Reilly C.F., Baugh R., Powers J.;  
 RT (in) Protein degradation in health and disease, Ciba Foundation  
 RT Symposium, pp.75:51-68, Excerpta Medica, Amsterdam and Oxford (1980).  
 RN [111]  
 RN SEQUENCE OF 30-49.  
 RA MEDLINE=89315847; PubMed=2501794;  
 RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,  
 RA Marra M.N., Seeger M., Nathan C.F.;  
 RT "Antibiotic proteins of human polymorphonuclear leukocytes."; *Proc. Natl. Acad. Sci. U.S.A.* 86:5610-5614(1989).  
 RN [112]  
 RN X-RAY CRYSTALLOGRAPHY (1.84 ANGSTROMS).  
 RA MEDLINE=89098932; PubMed=2911584;  
 RA Navia M.A., McKeever B.M., Springer J.P., Lin T.-Y., Williams H.R.,  
 RA Pluder E.M., Dorn C.P., Hoogsteen K.;  
 RT "Structure of human neutrophil elastase in complex with a peptide  
 RT chromomethyl ketone inhibitor at 1.84-A resolution."; *Proc. Natl. Acad. Sci. U.S.A.* 86:7-11(1989).  
 RN [113]  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RA MEDLINE=86271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;  
 RT "The refined 2.3-A crystal structure of human leukocyte elastase in a  
 RT complex with a valine chloromethyl ketone inhibitor."; *FEBS Lett.* 234:367-373(1988).  
 RN [114]  
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
 RA MEDLINE=87053808; PubMed=3640709;  
 RA Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;  
 RT "X-ray crystal structure of the complex of human leukocyte elastase  
 RT (P4M elastase) and the third domain of the turkey ovomucoid  
 RT inhibitor."; *EMBO J.* 5:2453-2458(1986).  
 RN [115]  
 RN VARIANTS CH VAL-32; PHE-177 AND GLN-191.  
 RA MEDLINE=20047772; PubMed=10581030; DOI=10.1038/70544;  
 RA Horwitz M., Benson K.F., Person R.E., Aprikyan A.G., Dale D.C.;  
 RT "Mutations in ELA2, encoding neutrophil elastase, define a 21-day  
 RT biological clock in cyclic haematopoiesis."; *Nat. Genet.* 23:433-436(1999).  
 CC -1- FUNCTION: Medullasin modifies the functions of natural killer  
 CC cells, monocytes and granulocytes.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins, including elastin.  
 CC Preferential cleavage: Val-I-Xaa > Ala-I-Xaa.  
 CC -1- TISSUE SPECIFICITY: Bone marrow cells.  
 CC -1- DISORD: Defects in ELA2 are a cause of cyclic haematopoiesis (CH)  
 CC [MIM:162800]; also known as cyclic neutropenia. CH is an autosomal

CC dominant disease in which blood-cell production from the bone  
 CC marrow oscillates with 21-day periodicity. Circulating neutrophils  
 CC vary between almost normal numbers and zero. During intervals of  
 CC neutropenia, affected individuals are at risk for opportunistic  
 CC infection. Monocytes, platelets, lymphocytes and reticulocytes  
 CC also cycle with the same frequency.  
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Elastase  
 CC subfamily.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: J03545; AAA52378.1; -;  
 DR EMBL: Y00477; CAA68537.1; -;  
 DR EMBL: X05875; CAA29299.1; -;  
 DR EMBL: X05875; CAA29300.1; ALT\_INIT.  
 DR EMBL: M20203; AAA36359.1; JOINED.  
 DR EMBL: M20199; AAA36359.1; JOINED.  
 DR EMBL: M20200; AAA36359.1; JOINED.  
 DR EMBL: AY596461; AAS89303.1; -;  
 DR EMBL: M34379; AAA36173.1; -;  
 DR EMBL: D00187; BAA00128.1; -;  
 DR PIR: A31976; ELHUL.  
 DR PDB: 1BOF; X-ray; A=30-247.  
 DR PDB: 1H1B; X-ray; A/B=30-247.  
 DR PDB: 1HNE; X-ray; E=30-247.  
 DR PDB: 1PPF; X-ray; E=30-247.  
 DR PDB: 1PPG; X-ray; E=30-247.  
 DR MEROPS: S01.131; -;  
 DR Genew: HGNC:3509; ELA2.  
 DR MIM: 130130; -;  
 DR MIM: 162800; -;  
 DR GO: GO:0004234; F:macrophage elastase activity; TMS.  
 DR InterPro: IPR009003; Pept\_Ser\_Cys.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR00114; Peptidase\_S1A.  
 DR Pfam: PF00089; Trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KW 3D-structure; Direct protein sequencing; Disease mutation;  
 KW Glycoprotein; Hydroxylase; Polymorphism; Serine protease; Signal.  
 FT SIGNAL 1 27  
 FT PROPEP 28 29  
 FT CHAIN 30 267  
 FT ACT\_SITE 30 70  
 FT ACT\_SITE 117 117  
 FT ACT\_SITE 202 202  
 FT ACT\_SITE 55 71  
 FT DISULFID 151 208  
 FT DISULFID 181 187  
 FT DISULFID 198 223  
 FT CARBOHYD 88 88  
 FT CARBOHYD 124 124  
 FT CARBOHYD 173 173  
 FT VARIANT 32 32  
 FT VARIANT 177 177  
 FT VARIANT 191 191  
 FT VARIANT 219 219  
 FT VARIANT 257 257  
 FT VARIANT 262 262  
 N-linked (GLCNAc . .) (Potential).  
 N-linked (GLCNAc . .).  
 N-linked (GLCNAc . .).  
 G -> V (in CH).  
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 V -> F (in CH).  
 /FTId=VAR\_009539.  
 R -> Q (in CH).  
 /FTId=VAR\_009540.  
 V -> I.  
 /FTId=VAR\_019237.  
 P -> L.  
 /FTId=VAR\_019238.  
 P -> L.  
 Leukocyte elastase.  
 Charge relay system.  
 Charge relay system.  
 Charge relay system.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 24, 2005, 13:01:06 ; Search time 170 Seconds

(without alignments)  
498.238 Million cell updates/sec

Title: US-10-733-288B-4

Perfect score: 1142

Sequence: 1 IVEGRARRAPAPFPMWSLDQ.....PDAPAPVAGFVNMDSIIQR 219

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum March 0%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*\n2: geneseqp1990s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1142	100.0	238	7	ADJ68391 Human hea
2	1142	100.0	247	4	ABBS5525 Human ela
3	1142	100.0	267	1	AAP80335 Sequence
4	1142	100.0	267	2	AAW64262 Human neu
5	1142	100.0	267	8	ADK42607 Human neu
6	1132	99.1	218	7	ADJ68281 Human hea
7	1123	98.3	218	5	AAU75897 Human leu
8	1073	94.0	257	5	ABP69417 Human pol
9	880.5	77.1	265	2	AAW70534 Human neu
10	877.5	76.8	265	2	AAW82629 Human ser
11	648.5	56.8	256	2	AAW85639 MY17 prep
12	648.5	56.8	256	7	ABW02656 Human pre
13	647.5	56.7	229	7	ABW02654 Human mat
14	647.5	56.7	256	2	AAW45403 Human ded
15	647.5	56.7	256	2	ABW02646 Human pre
16	647.5	56.7	256	8	ADM67204 Human hom
17	646.5	56.6	229	7	ABW02679 Human mat
18	644.5	56.4	229	7	ABW02678 Human mat
19	644.5	56.4	253	8	ADM67203 Murine ad
20	643.5	56.3	229	7	ABW02676 Human mat
21	642.5	56.3	229	7	ABW02677 Human mat
22	641.5	56.2	229	7	ABW02680 Human mat
23	641.5	56.2	237	2	AAW20509 Human pro
24	641.5	56.2	256	5	ABW06770 Human pro
25	641.5	56.2	256	8	ADQ14416 Human mye

26	641.5	56.2	256	8	ADR41702 Wegener's
27	578.5	50.7	215	2	AAR13036 Aar1036 Myeloblas
28	494.5	43.3	255	8	AD116330 Aar15330 Human pro
29	494	43.3	222	2	AAW73210 CAP37 pro
30	492	43.1	225	7	ADE11551 Aar11551 Human mat
31	490	42.9	225	3	AAW71881 Human hep
32	489	42.8	222	2	AAW41935 Recombina
33	489	42.8	232	7	ADG42088 Aar41935 Human pol
34	489	42.8	225	2	AAW88362 Human mat
35	489	42.8	225	2	AAW21551 Aar21551 Human hep
36	489	42.8	225	2	AAW88118 Aar88118 Mature hu
37	489	42.8	225	3	AAW71883 Human hep
38	489	42.8	225	3	AAW71876 Human mat
39	489	42.8	225	4	AAW71891 Human mat
40	489	42.8	225	7	ADE11587 Aar11587 Human mat
41	489	42.8	225	8	ADK42019 Aar42019 Human hep
42	489	42.8	232	2	AAW88364 Aar88364 Human pro
43	489	42.8	232	2	AAW21550 Aar21550 Human hep
44	489	42.8	232	2	AAW88120 Aar88120 Human hep
45	489	42.8	232	3	AAW71877 Aar71877 Human pre

#### ALIGNMENTS

RESULT 1  
ADJ68391  
ID ADJ68391 standard; protein; 238 AA.  
XX  
AC ADJ68391;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DS Human heat mitochondrial protein as a therapeutic target SegID197.  
XX  
KW mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotection; nocturnal; antidiabetic; anticonvulsant; antidiabetic; cytostatic.  
XX  
OS Homo sapiens.  
XX  
FN WO2003087768-A2.  
XX  
PD 23-OCT-2003.  
XX  
PE 04-APR-2003; 2003WC-US010870.  
XX  
PF 12-APR-2002; 2002US-0372843P.  
XX  
PR 17-JUN-2002; 2002US-0389987P.  
XX  
PR 20-SEP-2002; 2002US-0412418P.  
XX  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
XX  
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
PI Warnock DE;  
XX  
DR WPI; 2003-845369/78.  
XX  
PT Identifying a mitochondrial target for drug screening assays and for  
PT treating diseases associated with altered mitochondrial function,  
PT comprising detecting a modified polypeptide in a sample and correlating  
PT with the disease.  
PS Claim 1; SEQ ID NO 197; 180pp: English.  
XX  
CC This invention relates to novel mitochondrial targets that can be used  
CC for therapeutic intervention in treating a disease associated with  
CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, neurotropic, antidiabetic,  
CC anticonvulsant, antirheumatic, osteoprotic, ophthalmological and  
CC cytoskeletal activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.

SQ Sequence 238 AA;

Query Match 100.0%; Score 1142; DB 7; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.8e-67;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGRRARPHAMPFVMSIQLRGHEFCATLLAPNFVMSAHCVANVNVRAVVLGAHNL 60  
DB 1 IVGRRARPHAMPFVMSIQLRGHEFCATLLAPNFVMSAHCVANVNVRAVVLGAHNL 60  
QY 61 SRREPTROVFAVQRIFFENGYPVNLINDIVIIQLNGSATINNAVQAQLPAQGRRLGNGV 120  
DB 61 SRREPTROVFAVQRIFFENGYPVNLINDIVIIQLNGSATINNAVQAQLPAQGRRLGNGV 120  
QY 121 QCLANGWGLLGRNRGIAVLOELNVTVTSLCRSNVCTLVGRGAGVCFGSGSPLVCN 180  
DB 121 QCLANGWGLLGRNRGIAVLOELNVTVTSLCRSNVCTLVGRGAGVCFGSGSPLVCN 180  
QY 181 GLIHGIASFVRGCGASGLYPDAFAPVPAQFVNMWDSIIQR 219  
DB 181 GLIHGIASFVRGCGASGLYPDAFAPVPAQFVNMWDSIIQR 219

RESULT 2  
AAB55525  
ID AAB55525 standard; protein; 247 AA.  
XX

AC AAB55525;

XX 07-MAR-2001 (first entry)

DE Human elastase variant protein SEQ ID NO:95.

KM Human; elastase; variant; substrate; mutant; mutagenesis; histidine;  
KW human neutrophil elastase; H43A; cytoskeletal; proteolysis; ADAPT;  
XX antibody-directed enzyme activated prodrug therapy.

OS Homo sapiens.

PN WO200066363-A2.

PD 16-NOV-2000.

PF 04-MAY-2000; 2000WO-US006692.

PR 05-MAY-1999; 99US-0132640P.

PA (GETH ) GENENTECH INC.

PI Carter PJ, Dall'acqua W, Rodrigues M;

DR MPI: 2001-007389/01.

XX N-PSDB; AAC88022.

PT Elastase variant (H43A) having altered substrate specificity useful for  
XX antibody-directed enzyme activated prodrug therapy.

PS Disclosure; Fig 2; 79pp; English.

XX The present invention describes a purified elastase variant (I) with an

CC amino acid sequence different from that of a precursor elastase, the  
CC difference comprising a substitution of an active site histidine residue  
CC corresponding to residue 43 in human neutrophil elastase with a different  
CC amino acid residue so that (I) has substrate specificity substantially  
CC different from the precursor elastase. (I) has cytoskeletal activity, and  
CC can be used in antibody-directed enzyme activated prodrug therapy. The  
CC elastase variant can be used to cleave a particular substrate, especially  
CC those containing histidine residues at the substrate site. Site-specific  
CC proteolysis is useful in therapeutic applications, e.g. for antibody-  
CC directed enzyme activated prodrug therapy (ADAPT). AAC88022, AAC88023 and  
CC AAB55432 to AAB55526 represent sequences used in the exemplification of  
CC the present invention

SQ Sequence 247 AA;

Query Match 100.0%; Score 1142; DB 4; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.9e-67;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGRRARPHAMPFVMSIQLRGHEFCATLLAPNFVMSAHCVANVNVRAVVLGAHNL 60  
DB 5 IVGRRARPHAMPFVMSIQLRGHEFCATLLAPNFVMSAHCVANVNVRAVVLGAHNL 64  
QY 61 SRREPTROVFAVQRIFFENGYPVNLINDIVIIQLNGSATINNAVQAQLPAQGRRLGNGV 120  
DB 65 SRREPTROVFAVQRIFFENGYPVNLINDIVIIQLNGSATINNAVQAQLPAQGRRLGNGV 124  
QY 121 QCLANGWGLLGRNRGIAVLOELNVTVTSLCRSNVCTLVGRGAGVCFGSGSPLVCN 180  
DB 125 QCLANGWGLLGRNRGIAVLOELNVTVTSLCRSNVCTLVGRGAGVCFGSGSPLVCN 184  
QY 181 GLIHGIASFVRGCGASGLYPDAFAPVPAQFVNMWDSIIQR 219  
DB 185 GLIHGIASFVRGCGASGLYPDAFAPVPAQFVNMWDSIIQR 223

RESULT 3  
AAP80335  
ID AAP80335 standard; protein; 267 AA.  
XX

AC AAP80335;

XX 25-MAR-2003 (revised)

DT 04-OCT-1990 (first entry)

DE Sequence of serine protease (SP) of human myeloid cell origin and leader

DE peptide.

KW Serine protease; myeloid cell; intravascular coagulation treatment;  
XX enzyme.

OS Homo sapiens.

PN Key Location/Qualifiers

FT Peptide 1..29

PN Protein 30..267

PN WO8806621-A.

PD 07-SEP-1988.

PF 26-FEB-1988; 88WO-JP000205.

PR 05-MAR-1987; 87JP-00050676.

PR 09-SEP-1987; 87JP-00225540.

PA (TORA ) TORAY IND INC.

PI (AOKI/) AOKI Y.

XX Aoki Y, Okano K, Naruto M, Shimizu H, Nakamura H;  
DR MPI: 1988-271161/38.  
XX N-PSDB; AAP80315.

Mon Oct 24 14:14:59 2005

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 24, 2005, 12:59:58 : Search time 42 Seconds  
(without alignments)  
389,242 Million cell updates/sec

Title: US-10-733-288b-4

Perfect score: 1142

Sequence: 1 IVGGRARRAHMPFVWSLQL.....PDAPFVAQFVWIDSIQR 219

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1142	100.0	238	3 US-08-944-483-31	Sequence 31, Appl
2	1142	100.0	238	6 5180819-4	Patent No. 5180819
3	1142	100.0	238	6 5180819-4	Patent No. 5180819
4	1142	100.0	257	2 US-08-978-404B-46	Sequence 46, Appl
5	792	69.4	271	3 US-09-578-303-6	Sequence 6, Appl
6	648.5	56.8	229	4 US-08-395-456C-27	Sequence 27, Appl
7	648.5	56.8	221	4 US-08-395-456C-25	Sequence 25, Appl
8	648.5	56.8	256	4 US-08-395-456C-23	Sequence 23, Appl
9	648.5	56.8	229	2 US-08-487-453A-23	Sequence 23, Appl
10	647.5	56.7	229	2 US-08-394-600B-20	Sequence 20, Appl
11	647.5	56.7	229	4 US-08-395-456C-20	Sequence 20, Appl
12	647.5	56.7	229	4 US-08-487-453A-20	Sequence 20, Appl
13	647.5	56.7	229	5 PCT-US95-02513-20	Sequence 20, Appl
14	647.5	56.7	229	2 US-08-230-428B-4	Sequence 4, Appl
15	641.5	56.2	229	3 US-08-944-483-30	Sequence 30, Appl
16	641.5	56.2	256	4 US-09-949-016-6271	Sequence 6271, Ap
17	590	51.7	214	6 5180819-3	Patent No. 5180819
18	590	51.7	214	6 5180819-3	Patent No. 5180819
19	581.5	50.9	215	6 5180819-2	Patent No. 5180819
20	581.5	50.9	215	6 5180819-2	Patent No. 5180819
21	494	43.3	222	2 US-08-491-204A-18	Sequence 18, Appl
22	489	42.8	232	1 US-07-969-931-9	Sequence 9, Appl
23	489	42.8	225	3 US-07-855-417A-9	Sequence 9, Appl
24	489	42.8	225	3 US-08-944-483-32	Sequence 32, Appl
25	489	42.8	251	4 US-09-949-016-6112	Sequence 6112, Ap
26	489	42.8	255	4 US-09-949-016-9690	Sequence 9690, Ap
27	486	42.6	221	2 US-08-925-708-1	Sequence 1, Appl

28	433	37.9	219	2	US-08-925-708-2	Sequence 2, Appl
29	381	33.4	283	4	US-09-244-111-2	Sequence 2, Appl
30	377	33.0	240	1	US-08-278-091-11	Sequence 11, Appl
31	377	33.0	240	1	US-08-483-859-11	Sequence 11, Appl
32	377	33.0	240	1	US-08-472-173-11	Sequence 11, Appl
33	377	33.0	240	2	US-08-487-167-11	Sequence 11, Appl
34	377	33.0	240	2	US-08-482-816-11	Sequence 11, Appl
35	377	33.0	240	2	US-08-296-149-11	Sequence 11, Appl
36	377	33.0	240	2	US-08-801-499-11	Sequence 11, Appl
37	377	33.0	240	2	US-08-615-271-11	Sequence 11, Appl
38	377	33.0	240	3	US-09-074-660-11	Sequence 11, Appl
39	377	33.0	240	3	US-09-074-659-11	Sequence 11, Appl
40	377	33.0	240	3	US-09-106-468-11	Sequence 11, Appl
41	377	33.0	240	3	US-09-106-465A-11	Sequence 11, Appl
42	377	33.0	240	3	US-09-106-467-11	Sequence 11, Appl
43	364	31.9	133	4	US-09-949-016-7471	Sequence 7471, Ap
44	351.5	30.8	234	3	US-08-944-483-46	Sequence 46, Appl
45	351.5	30.8	268	4	US-09-949-016-10712	Sequence 10712, A

## ALIGNMENTS

RESULT 1  
US-08-944-483-31  
Sequence 31, Application US/08944483  
Patent No. 6232456  
GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLAS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
TITLE OF INVENTION: OF THE PROSTATE  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 238 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: No. 62324566  
US-08-944-483-31

Query Match 100.0%; Score 1142; DB 3; Length 238;  
Best Local Similarity 100.0%; Pred. No. 3,7e-123;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRRARPHAMPFWVSILQIRGHEFCGATLLAPNFVMSAAHCVANNVRAVVLGAHNL 60  
DB 1 IVGGRRARPHAMPFWVSILQIRGHEFCGATLLAPNFVMSAAHCVANNVRAVVLGAHNL 60  
QY 61 SRRPTROYFAVQRIFFENGYPDVLNLDIVIIQLNGSATINNAVQALPAQGRRLGNGV 120  
DB 61 SRRPTROYFAVQRIFFENGYPDVLNLDIVIIQLNGSATINNAVQALPAQGRRLGNGV 120  
QY 121 QCLANGWGLGRRNRGIAVLOELNVTVTSICRRSNVCTLVGRQAGVCFGDSGPLVCN 180  
DB 121 QCLANGWGLGRRNRGIAVLOELNVTVTSICRRSNVCTLVGRQAGVCFGDSGPLVCN 180  
QY 181 GLIHGIASFVRGCGASGLYPDAFAPVAQFVNMIDSIQR 219  
DB 181 GLIHGIASFVRGCGASGLYPDAFAPVAQFVNMIDSIQR 219

## RESULT 2

5180819-4  
PATENT No. 5180819  
APPLICANT: CAYRE, YVON  
TITLE OF INVENTION: PURIFIED MYELOBLASTIN, NUCLEIC ACID  
MOLECULE ENCODING SAME, AND USES THEREOF  
NUMBER OF SEQUENCES: 9  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/455,614  
FILING DATE: 22-DEC-1989  
SEQ ID NO:4:  
LENGTH: 238  
5180819-4

Query Match 100.0%; Score 1142; DB 6; Length 238;  
Best Local Similarity 100.0%; Pred. No. 3,7e-123;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRRARPHAMPFWVSILQIRGHEFCGATLLAPNFVMSAAHCVANNVRAVVLGAHNL 60  
DB 1 IVGGRRARPHAMPFWVSILQIRGHEFCGATLLAPNFVMSAAHCVANNVRAVVLGAHNL 60  
QY 61 SRRPTROYFAVQRIFFENGYPDVLNLDIVIIQLNGSATINNAVQALPAQGRRLGNGV 120  
DB 61 SRRPTROYFAVQRIFFENGYPDVLNLDIVIIQLNGSATINNAVQALPAQGRRLGNGV 120  
QY 121 QCLANGWGLGRRNRGIAVLOELNVTVTSICRRSNVCTLVGRQAGVCFGDSGPLVCN 180  
DB 121 QCLANGWGLGRRNRGIAVLOELNVTVTSICRRSNVCTLVGRQAGVCFGDSGPLVCN 180  
QY 181 GLIHGIASFVRGCGASGLYPDAFAPVAQFVNMIDSIQR 219  
DB 181 GLIHGIASFVRGCGASGLYPDAFAPVAQFVNMIDSIQR 219

## RESULT 3

5180819-4  
PATENT No. 5180819  
APPLICANT: CAYRE, YVON  
TITLE OF INVENTION: PURIFIED MYELOBLASTIN, NUCLEIC ACID  
MOLECULE ENCODING SAME, AND USES THEREOF  
NUMBER OF SEQUENCES: 9  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/455,614  
FILING DATE: 22-DEC-1989  
SEQ ID NO:4:  
LENGTH: 238  
5180819-4

Query Match 100.0%; Score 1142; DB 6; Length 238;  
Best Local Similarity 100.0%; Pred. No. 3,7e-123;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRRARPHAMPFWVSILQIRGHEFCGATLLAPNFVMSAAHCVANNVRAVVLGAHNL 60  
DB 1 IVGGRRARPHAMPFWVSILQIRGHEFCGATLLAPNFVMSAAHCVANNVRAVVLGAHNL 60  
QY 61 SRRPTROYFAVQRIFFENGYPDVLNLDIVIIQLNGSATINNAVQALPAQGRRLGNGV 120  
DB 61 SRRPTROYFAVQRIFFENGYPDVLNLDIVIIQLNGSATINNAVQALPAQGRRLGNGV 120  
QY 121 QCLANGWGLGRRNRGIAVLOELNVTVTSICRRSNVCTLVGRQAGVCFGDSGPLVCN 180  
DB 121 QCLANGWGLGRRNRGIAVLOELNVTVTSICRRSNVCTLVGRQAGVCFGDSGPLVCN 180  
QY 181 GLIHGIASFVRGCGASGLYPDAFAPVAQFVNMIDSIQR 219  
DB 181 GLIHGIASFVRGCGASGLYPDAFAPVAQFVNMIDSIQR 219

## RESULT 4

US-08-978-404B-46  
Sequence 46, Application US/08978404B

PATENT No. 5968782  
GENERAL INFORMATION:  
APPLICANT: Stevens, Richard L.  
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02210-2211  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,404B  
FILING DATE: 25-NOV-97  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/032,354  
FILING DATE: 04-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7090  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
TELEX:  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5968782e  
US-08-978-404B-46

Query Match 100.0%; Score 1142; DB 2; Length 267;  
Best Local Similarity 100.0%; Pred. No. 4,3e-123;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRRARPHAMPFWVSILQIRGHEFCGATLLAPNFVMSAAHCVANNVRAVVLGAHNL 60  
DB 30 IVGGRRARPHAMPFWVSILQIRGHEFCGATLLAPNFVMSAAHCVANNVRAVVLGAHNL 89



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 24, 2005, 12:59:58 ; Search time 164 Seconds  
(without alignments)  
557.524 Million cell updates/sec

Title: US-10-733-288B-4

Perfect score: 1142

Sequence: 1 IVGGRRARHPFMVSLQ.....PDAFPAVQFVMWIDSIQR 219

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1862986 seqs, 417506248 residues

Total number of hits satisfying chosen parameters: 1862986

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/prodata/1/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubppa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubppa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/1/pubppa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*  
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11: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*  
12: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
16: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
17: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
18: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
19: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
20: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
21: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/prodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1142	100.0	238	11	US-09-789-210-31
2	1142	100.0	238	16	US-10-408-765A-197
3	1142	100.0	240	18	US-10-970-794-8
4	1142	100.0	267	17	US-10-931-153-22
5	1142	100.0	267	18	US-10-970-794-7
6	1133	99.2	219	16	US-10-733-288A-4
7	1132	99.2	218	16	US-10-408-765A-87
8	1123	98.3	218	9	US-09-861-708-3
9	1114	97.5	218	16	US-10-733-288A-3
10	641.5	56.2	229	11	US-09-789-210-30
11	489	42.8	222	15	US-10-423-311-1

12	489	42.8	225	11	US-09-789-210-32	Sequence 32, Appl
13	489	42.8	225	17	US-10-868-577A-30	Sequence 30, Appl
14	489	42.8	225	17	US-10-868-577A-38	Sequence 38, Appl
15	425	37.2	199	14	US-10-384-474-8	Sequence 8, Appl
16	425	37.0	199	15	US-10-423-311-2	Sequence 2, Appl
17	385	33.7	284	9	US-09-888-615-112	Sequence 112, Appl
18	381	33.4	283	10	US-09-946-374-111	Sequence 111, Appl
19	381	33.4	283	13	US-10-052-568-272	Sequence 272, Appl
20	381	33.4	283	14	US-10-174-599-272	Sequence 272, Appl
21	381	33.4	283	14	US-10-176-788-272	Sequence 272, Appl
22	381	33.4	283	14	US-10-175-737-272	Sequence 272, Appl
23	381	33.4	283	14	US-10-174-583-272	Sequence 272, Appl
24	381	33.4	283	14	US-10-176-483-272	Sequence 272, Appl
25	381	33.4	283	14	US-10-176-749-272	Sequence 272, Appl
26	381	33.4	283	14	US-10-176-914-272	Sequence 272, Appl
27	381	33.4	283	14	US-10-176-915-272	Sequence 272, Appl
28	381	33.4	283	14	US-10-173-706-272	Sequence 272, Appl
29	381	33.4	283	14	US-10-175-738-272	Sequence 272, Appl
30	381	33.4	283	14	US-10-175-752-272	Sequence 272, Appl
31	381	33.4	283	14	US-10-176-482-272	Sequence 272, Appl
32	381	33.4	283	14	US-10-176-757-272	Sequence 272, Appl
33	381	33.4	283	14	US-10-176-913-272	Sequence 272, Appl
34	381	33.4	283	14	US-10-180-552-272	Sequence 272, Appl
35	381	33.4	283	14	US-10-180-557-272	Sequence 272, Appl
36	381	33.4	283	14	US-10-173-700-272	Sequence 272, Appl
37	381	33.4	283	14	US-10-174-572-272	Sequence 272, Appl
38	381	33.4	283	14	US-10-174-579-272	Sequence 272, Appl
39	381	33.4	283	14	US-10-174-582-272	Sequence 272, Appl
40	381	33.4	283	14	US-10-174-588-272	Sequence 272, Appl
41	381	33.4	283	14	US-10-175-739-272	Sequence 272, Appl
42	381	33.4	283	14	US-10-175-740-272	Sequence 272, Appl
43	381	33.4	283	14	US-10-176-488-272	Sequence 272, Appl
44	381	33.4	283	14	US-10-176-492-272	Sequence 272, Appl
45	381	33.4	283	14	US-10-176-492-272	Sequence 272, Appl

## ALIGNMENTS

RESULT 1  
US-09-789-210-31  
Sequence 31, Application US/09789210  
Publication No. US20040241646A1

GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
COLPITTS, TRACEY L.  
FRIEDMAN, PAULA N.  
GRANADOS, EDWARD N.  
KLASS, MICHAEL R.  
RUSSELL, JOHN C.  
STEWART, KENT D.  
STROUPE, STEVEN D.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES OF THE PROSTATE

NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTEST for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/789, 210  
FILING DATE: 20-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/944,483  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 238 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: None  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-789-210-31

Query Match 100.0%; Score 1142; DB 11; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.3e-110;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGRRARPHAMPFVMSIQLRGHCATLLIAPNFVMSAAHCVANVNVRAVVLGAHNL 60  
DB 1 IVGRRARPHAMPFVMSIQLRGHCATLLIAPNFVMSAAHCVANVNVRAVVLGAHNL 60  
QY 61 SRREPTROVFAVORIFENGYPDVLNDIVILQLNGSATINNAVVOALPAQGRRLGNGV 120  
DB 61 SRREPTROVFAVORIFENGYPDVLNDIVILQLNGSATINNAVVOALPAQGRRLGNGV 120  
QY 121 OCLANGWGLGRNRGIASVLOELNVTVTSLCRSNVCTLVGRGAGVCFDGSGLPVLCN 180  
DB 121 OCLANGWGLGRNRGIASVLOELNVTVTSLCRSNVCTLVGRGAGVCFDGSGLPVLCN 180  
QY 181 GLIHGIASFVRGCGASGLYPDAFAPVAPQFVNMWIDSIIR 219  
DB 181 GLIHGIASFVRGCGASGLYPDAFAPVAPQFVNMWIDSIIR 219

RESULT 2  
US-10-408-765A-197  
Sequence 197, Application US/10408765A  
Publication No. US20040101874A1  
GENERAL INFORMATION:  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Rany, Bojin D.  
APPLICANT: Zhang, Bing  
APPLICANT: Gibson, Bradford W.  
APPLICANT: Taylor, Steven W.  
APPLICANT: Glenn, Gary M.  
APPLICANT: Marnock, Dale E.  
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
FILE REFERENCE: 660088.465  
CURRENT APPLICATION NUMBER: US/10/408,765A  
CURRENT FILING DATE: 2003-04-04  
NUMBER OF SEQ ID NOS: 3077  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 197  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-408-765A-197

Query Match 100.0%; Score 1142; DB 16; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.3e-110;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGRRARPHAMPFVMSIQLRGHCATLLIAPNFVMSAAHCVANVNVRAVVLGAHNL 60  
DB 1 IVGRRARPHAMPFVMSIQLRGHCATLLIAPNFVMSAAHCVANVNVRAVVLGAHNL 60

QY 61 SRREPTROVFAVORIFENGYPDVLNDIVILQLNGSATINNAVVOALPAQGRRLGNGV 120  
DB 61 SRREPTROVFAVORIFENGYPDVLNDIVILQLNGSATINNAVVOALPAQGRRLGNGV 120  
QY 121 OCLANGWGLGRNRGIASVLOELNVTVTSLCRSNVCTLVGRGAGVCFDGSGLPVLCN 180  
DB 121 OCLANGWGLGRNRGIASVLOELNVTVTSLCRSNVCTLVGRGAGVCFDGSGLPVLCN 180  
QY 181 GLIHGIASFVRGCGASGLYPDAFAPVAPQFVNMWIDSIIR 219  
DB 181 GLIHGIASFVRGCGASGLYPDAFAPVAPQFVNMWIDSIIR 219

RESULT 3  
US-10-970-794-8  
Sequence 8, Application US/10970794  
Publication No. US20050136398A1  
GENERAL INFORMATION:  
APPLICANT: McDermott, Martin  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING THERAPEUTIC COMPOUNDS  
FILE REFERENCE: 18477.043  
CURRENT APPLICATION NUMBER: US/10/970,794  
PRIOR FILING DATE: 2004-10-22  
PRIOR APPLICATION NUMBER: 60/514,241  
PRIOR FILING DATE: 2003-10-24  
PRIOR APPLICATION NUMBER: 60/514,299  
PRIOR FILING DATE: 2003-10-24  
PRIOR APPLICATION NUMBER: 60/513,532  
PRIOR FILING DATE: 2003-10-24  
PRIOR APPLICATION NUMBER: 60/513,542  
PRIOR FILING DATE: 2003-10-24  
PRIOR APPLICATION NUMBER: 60/514,894  
PRIOR FILING DATE: 2003-10-29  
PRIOR APPLICATION NUMBER: 60/514,925  
PRIOR FILING DATE: 2003-10-29  
PRIOR APPLICATION NUMBER: To Be Assigned  
PRIOR FILING DATE: 2004-10-22  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 240  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-970-794-8

Query Match 100.0%; Score 1142; DB 18; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1.3e-110;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGRRARPHAMPFVMSIQLRGHCATLLIAPNFVMSAAHCVANVNVRAVVLGAHNL 60  
DB 3 IVGRRARPHAMPFVMSIQLRGHCATLLIAPNFVMSAAHCVANVNVRAVVLGAHNL 62  
QY 61 SRREPTROVFAVORIFENGYPDVLNDIVILQLNGSATINNAVVOALPAQGRRLGNGV 120  
DB 61 SRREPTROVFAVORIFENGYPDVLNDIVILQLNGSATINNAVVOALPAQGRRLGNGV 122  
QY 121 OCLANGWGLGRNRGIASVLOELNVTVTSLCRSNVCTLVGRGAGVCFDGSGLPVLCN 180  
DB 121 OCLANGWGLGRNRGIASVLOELNVTVTSLCRSNVCTLVGRGAGVCFDGSGLPVLCN 182  
QY 181 GLIHGIASFVRGCGASGLYPDAFAPVAPQFVNMWIDSIIR 219  
DB 181 GLIHGIASFVRGCGASGLYPDAFAPVAPQFVNMWIDSIIR 221

RESULT 4  
US-10-931-153-22  
Sequence 22, Application US/10931153  
Publication No. US20050089515A1  
GENERAL INFORMATION:  
APPLICANT: Ley, Arthur C.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 24, 2005, 13:09:21 ; Search time 39 Seconds  
(without alignments)  
540.294 Million cell updates/sec

Title: US-10-733-288b-4

Perfect score: 1142  
Sequence: 1 IVGGRARRAHMPFVMSLQ.....PDARFVAQFVWMDISLIR 219

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR 79:.\*  
2: PIR:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	1142	100.0	267	1	ELHUL leukocyte elastase
2	873.5	76.5	265	2	neutrophil elastase
3	646.5	56.6	256	1	PRHU3 proteinase 3 (EC 3
4	489	42.8	251	1	TRHUA2 azurocidin precurs
5	437	38.3	219	1	TRPGA2 azurocidin - pig
6	379	32.2	266	1	ELPG pancreatic elastase
7	368	32.2	258	4	S70439 pancreatic elastase
8	368	32.2	267	4	A56615 probable pancreati
9	365	31.0	266	1	ELRT1 pancreatic elastase
10	353.5	30.6	261	2	S40162 cathepsin G (EC 3.
11	351.5	30.6	262	1	A31372 granzyme A (EC 3.4
12	349.5	30.6	226	2	S69370 duodenase - bovine
13	346.5	30.3	255	2	A27122 cathepsin G (EC 3.
14	341	29.9	244	2	A34910 mast cell proteina
15	339.5	29.7	257	2	B45061 granzyme A (EC 3.4
16	339.5	29.7	260	2	A45061 granzyme A (EC 3.4
17	337.5	29.6	249	2	A55634 granzyme M (EC 3.4
18	336.5	29.5	269	2	A26023 pancreatic elastase
19	335.5	29.4	263	1	I55608 complement factor
20	335	29.3	258	2	I56220 trypsin 2 - rat
21	333.5	29.1	259	1	WMMS28 complement factor
22	332.5	29.2	271	1	ELRT2 pancreatic elastase
23	332	29.1	236	2	A28566 T-cell suppressor
24	332	29.1	246	1	DBHU complement factor
25	331.5	29.0	271	2	A25528 pancreatic elastase
26	329.5	28.9	251	2	T10262 mast cell serine p
27	329.5	28.9	265	2	T10495 chymotrypsin (EC 3
28	329.5	28.9	269	2	B26823 pancreatic elastase
29	329	28.8	244	2	A46721 chymase (EC 3.4.21

30	329	28.8	246	2	A36678 mast cell proteina
31	328.5	28.8	226	1	KCFP bradykinin (EC 3.4
32	322	28.2	258	2	A45161 serine proteinase
33	321	28.1	246	1	A46504 chymase (EC 3.4.21
34	321	28.1	810	1	PLHU plasmin (EC 3.4.21
35	320	28.0	268	2	S68825 pancreatic elastase
36	317	27.8	246	2	S64707 chymase (EC 3.4.21
37	316.5	27.7	271	2	S29239 chymotrypsin (EC 3
38	316.5	27.7	281	1	A61021 granzyme B (EC 3.4
39	315.5	27.6	812	1	PLBO plasmin (EC 3.4.21
40	312	27.3	247	2	S64708 chymase (EC 3.4.21
41	312	27.3	268	2	S68825 pancreatic elastase
42	312	27.3	455	2	A61545 plasmin (EC 3.4.21
43	312	27.3	810	2	B30848 plasmin (EC 3.4.21
44	311.5	27.3	810	2	I46260 plasmin (EC 3.4.21
45	310.5	27.2	243	2	A35871 trypsin (EC 3.4.21

## ALIGNMENTS

### RESULT 1

ELHUL  
leukocyte elastase (EC 3.4.21.37) precursor [validated] - human  
N:Alternate names: inflammatory serine proteinase; medullasin; neutrophil elastase  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1990 #sequence, revision 30-Jun-1990 #text change 09-Jul-2004  
C/Accession: A31976; S04954; S06241; A27064; S00631; A28370; A34570; A05293; A25907; S14  
J.Takahashi, H.; Nukitwa, T.; Yoshimura, K.; Quirk, C.D.; States, D.J.; Holmes, M.D.; Whar  
R. Biol. Chem. 263, 14739-14747, 1988  
A>Title: Structure of the human neutrophil elastase gene.  
A/Reference number: A31976; PMID:89008342; PMID:2902087  
A/Accession: A31976  
A/Molecule type: DNA  
A/Residues: 1-267 <TRAX>  
A/Cross-references: UNIPROT:P08246; GB:M20203; GB:J04032; NID:G189147; PIDN:AAA36359.1; I  
R/Fairley, D.; Travis, J.; Salvesen, G.  
Biol. Chem. Hoppe-Seyler 370, 737-744, 1989  
A>Title: The human neutrophil elastase gene. Analysis of the nucleotide sequence reveals  
A/Reference number: S04954; PMID:89374820; PMID:2775493  
A/Accession: S04954  
A/Status: not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-267 <FAR>  
R.Nakamura, H.; Okano, K.; Aoki, Y.; Shimizu, H.; Naruto, M.  
Nucleic Acids Res. 15, 9601-9602, 1987  
A>Title: Nucleotide sequence of human bone marrow serine protease (medullasin) gene.  
A/Reference number: S06241; PMID:88067782; PMID:3479752  
A/Accession: S06241  
A/Status: preliminary; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-267 <NAK>  
A/Cross-references: EMBL:Y00477; NID:G34529; PIDN:CAA68537.1; PID:G296665  
R/Okano, K.; Aoki, Y.; Sakurai, T.; Kajitani, M.; Kanai, S.; Shimizu, T.; Shimizu, H.; Ne  
J. Biochem. 102, 13-16, 1987  
A>Title: Molecular cloning of complementary DNA for human medullasin: an inflammatory ser  
A/Reference number: A27064; PMID:88022918; PMID:2822677  
A/Accession: A27064  
A/Molecule type: mRNA  
A/Residues: 30-267 <OKA>  
A/Cross-references: EMBL:X05875; NID:G34532; PIDN:CAA29300.1; PID:G1335212  
R/Fairley, D.; Salvesen, G.; Travis, J. 3-7, 1988  
Biol. Chem. Hoppe-Seyler 369(suppl.), 3-7, 1988  
A>Title: Molecular cloning of human neutrophil elastase.  
A/Reference number: S00631; PMID:89076526; PMID:2462434  
A/Accession: S00631  
A/Molecule type: mRNA  
A/Residues: 123-267 <FA2>  
A/Cross-references: GB:M27783; NID:G182055; PIDN:AAA35792.1; PID:G182056  
A/Note: the authors translated the codon TTC for residue 218 as Pro  
R.Takahashi, H.; Nukitwa, T.; Bassett, P.; Crystal, R.G.  
J. Biol. Chem. 263, 2543-2547, 1988

A>Title: Myelomonocytic cell lineage expression of the neutrophil elastase gene.  
 A:Reference number: A28370; MUID:88115408; PMID:3422232  
 A:Accession: A28370  
 A:Molecule type: mRNA  
 A:Residues: 75-267 <TA2>  
 A:Cross-references: GB:J03545; NID:9182050; PIDN:AAA52378.1; PID:9182051  
 B:Okano, K.; Aoki, Y.; Shimizu, H.; Naruto, M.  
 Biochem. Biophys. Res. Commun. 167, 1326-1332, 1990  
 A>Title: Functional expression of human leukocyte elastase (HLE)/medullasin in eukaryotic  
 A:Reference number: A35570; MUID:90211319; PMID:2322278  
 A:Accession: A35570  
 A:Molecule type: mRNA  
 A:Residues: 1-267 <OK2>  
 A:Cross-references: GB:M34379; NID:9187116; PIDN:AAA6173.1; PID:9307123  
 R:Travis, J.; Giles, P.J.; Porcelll, L.; Reilly, C.F.; Baugh, R.; Powers, J.  
 in Protein Degradation in Health and Disease, Ciba Foundation Symposium 75, 51-68, 1980  
 A:Reference number: A94428  
 A:Accession: A05293  
 A:Molecule type: protein  
 A:Residues: 30-66,'G','68-73','D','75,78-82','E','84-89','T','91-94','PT','97-100','L','102-103 <TR  
 A:Experimental source: neutrophil granulocytes  
 R:Simha, S.; Mawork, W.; Kart, S.; Giles, J.; Bode, W.; Travis, J.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 2228-2232, 1987  
 A>Title: Primary structure of human neutrophil elastase.  
 A:Reference number: A25907; MUID:87175647; PMID:3550808  
 A:Accession: A25907  
 A:Molecule type: protein  
 A:Residues: 30-247 <STN>  
 A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having 107-Asp  
 R:Green, B.G.; Weston, H.; Ashe, B.M.; Doherty, J.; Finke, P.; Hagmann, W.; Lark, M.; Ma  
 Arch. Biochem. Biophys. 266, 284-292, 1991  
 A>Title: PMN elastases: a comparison of the specificity of human isozymes and the enzyme  
 A:Reference number: S14736; MUID:91378304; PMID:1897955  
 A:Accession: S14736  
 A:Molecule type: protein  
 A:Residues: 30-50 <GRE>  
 C:Comment: This is a lysosomal proteinase found in the azurophilic granules of neutrophils  
 C:Comment: This elastase cleaves preferentially bonds after Ala and Val. It is believed  
 C:Genetics:  
 A:Gene: GDB:ELA2  
 A:Cross-references: GDB:118792; OMIM:130130  
 A:Map position: 19p13.3-19p13.3  
 A:Introns: 23/1; 75/2; 122/3; 199/3  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: emphysema; glycoprotein; hydrolysis; leukocyte; lysosome; rheumatoid arthritis  
 F.1-27/Domain: signal sequence #status predicted <STS>  
 F.28-29/Domain: propeptide #status predicted <PRO>  
 F.30-247/Product: leukocyte elastase #status experimental <MAT>  
 F.248-267/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
 F.55-71,151-208,181-187,198-223/Dissulfide bonds: #status experimental  
 F.70,117,202/Active site: His, Asp, Ser #status predicted  
 F.88/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F.124,173/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 1142; DB 1; Length 267;  
 Best Local Similarity 100.0%; Pred. No.1.1e-97;  
 Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRRARHPMPWVSLOLRGHEFCGATLIPNPFMSAAHCYANNVRAVRVIGAHNL 60  
 DB 30 IVGGRRARHPMPWVSLOLRGHEFCGATLIPNPFMSAAHCYANNVRAVRVIGAHNL 89  
 QY 61 SRREPTROFVAQRIFENGYPDVNLINDVILQNGSATINNVOVAOLPAGGRRLNGCV 120  
 DB 90 SRREPTROFVAQRIFENGYPDVNLINDVILQNGSATINNVOVAOLPAGGRRLNGCV 149  
 QY 121 OCLANGWGLGRNRGIAVLQELNVTVTSLCRSNVCTLVGRQAGVCFDGSGLPYCN 180  
 DB 150 OCLANGWGLGRNRGIAVLQELNVTVTSLCRSNVCTLVGRQAGVCFDGSGLPYCN 209  
 QY 181 GLIHGIASFVRGCGASGLYPDAFAPVAQFVNMWIDSIQR 219

DB 210 GLIHGIASFVRGCGASGLYPDAFAPVAQFVNMWIDSIQR 248  
 RESULT 2  
 148679  
 neutrophil elastase - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #txc\_change 09-Jul-2004  
 C:Accession: 148679  
 R:Nuchprayoon, I.; Meyers, S.; Scott, L.M.; Suzow, J.; Hiebert, S.; Friedman, A.D.  
 Mol. Cell. Biol. 14, 5558-5568, 1994  
 A>Title: FEEDP2/CBF, the murine homolog of the human myeloid AML1 and FEED2 beta/CBF beta  
 15.  
 A:Reference number: 148679; MUID:94309676; PMID:8035830  
 A:Accession: 148679  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-265 <RES>  
 A:Cross-references: UNIPROT:Q61515; EMBL:U04962; NID:9452556; PIDN:AAB60670.1; PID:945255  
 C:Genetics:  
 A:Introns: 22/1; 74/2; 121/3; 199/3  
 C:Superfamily: trypsin; trypsin homology  
 F.29-242/Domain: trypsin homology <TRI>

Query Match 76.5%; Score 873.5; DB 2; Length 265;  
 Best Local Similarity 75.9%; Pred. No.5.8e-73;  
 Matches 167; Conservative 20; Mismatches 33; Indels 1; Gaps 1;

QY 1 IVGGRRARHPMPWVSLOLRGHEFCGATLIPNPFMSAAHCYANNVRAVRVIGAHNL 60  
 DB 29 IVGGRRARHPMPWVSLOLRGHEFCGATLIPNPFMSAAHCYANNVRAVRVIGAHNL 88  
 QY 61 SRREPTROFVAQRIFENGYPDVNLINDVILQNGSATINNVOVAOLPAGGRRLNGCV 120  
 DB 89 SRREPTROFVAQRIFENGYPDVNLINDVILQNGSATINNVOVAOLPAGGRRLNGCV 148  
 QY 121 OCLANGWGLGRNRGIAVLQELNVTVTSLCRSNVCTLVGRQAGVCFDGSGLPYCN 179  
 DB 149 OCLANGWGLGRNRGIAVLQELNVTVTSLCRSNVCTLVGRQAGVCFDGSGLPYCN 208  
 QY 180 NGLIHGIASFVRGCGASGLYPDAFAPVAQFVNMWIDSIQR 219  
 DB 209 NGLIHGIASFVRGCGASGLYPDAFAPVAQFVNMWIDSIQR 248

RESULT 3  
 PNHU3  
 Proteinase 3 (EC 3.4.21.-) precursor [validated] - human  
 N:Alternate names: AGP7; C-ANCA antigen; neutrophil proteinase 4; p29; Wegener's granulo  
 N:Contains: myeloblastin  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #txc\_change 09-Jul-2004  
 C:Accession: A45080; B46268; A45983; JH0331; A33751; S11091; A61176; A60148; A43982; A43  
 R:Sturrock, A.B.; Franklin, K.F.; Rao, G.; Marshall, B.C.; Rebentisch, W.B.; Lemons, R.S.  
 J. Biol. Chem. 267, 21193-21199, 1992  
 A>Title: Structure, chromosomal assignment, and expression of the gene for proteinase-3.  
 A:Reference number: A45080; MUID:93016043; PMID:1400430  
 A:Accession: A45080  
 A:Molecule type: DNA  
 A:Residues: 1-254,'P' <STU>  
 A:Cross-references: UNIPROT:P24158; GB:M97911  
 A:Note: sequence extracted from NCBI backbone (NCBI:116205)  
 R:Zimmer, M.; Medcalf, R.L.; Fink, T.M.; Matzmann, C.; Lichter, P.; Jenne, D.E.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 8215-8219, 1992  
 A>Title: Three human elastase-like genes coordinately expressed in the myelomonocytic line  
 A:Reference number: A46268; MUID:92390417; PMID:1518849  
 A:Accession: B46268  
 A:Molecule type: DNA  
 A:Residues: 1-118,'V','120-134','AT','137-256 <ZIM>  
 A:Note: sequence extracted from NCBI backbone (NCBI:112898, NCBI:112900, NCBI:112902,  
 R:Labbaye, C.; Musette, P.; Cayre, Y.E.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 9253-9256, 1991  
 A>Title: Wegener autoantigen and myeloblastin are encoded by a single mRNA.